

> d his

(FILE 'HOME' ENTERED AT 09:32:43 ON 31 MAY 2006)

FILE 'AGRICOLA, MEDLINE, CAPIUS, BIOSIS' ENTERED AT 09:32:46 ON 31 MAY 2006

L1 10280 S RHODOCOCCUS  
L2 234 S L1 (10N) DEHYDROGENASE  
L3 156 DUP REM L2 (78 DUPLICATES REMOVED)  
L4 67 S L3 AND ALCOHOL  
L5 40 S L4 AND PY<2003  
L6 2 S L5 AND RUBER

FILE 'STNGUIDE' ENTERED AT 09:35:04 ON 31 MAY 2006

FILE 'AGRICOLA, MEDLINE, CAPIUS, BIOSIS' ENTERED AT 09:43:15 ON 31 MAY 2006

L7 12 S L3 AND RUBER  
L8 12 DUP REM L7 (0 DUPLICATES REMOVED)  
L9 113 S L3 AND PY<2003  
L10 4 S L8 AND PY<2003

FILE 'STNGUIDE' ENTERED AT 09:48:34 ON 31 MAY 2006

FILE 'AGRICOLA, MEDLINE, CAPIUS, BIOSIS' ENTERED AT 09:49:25 ON 31 MAY 2006

FILE 'STNGUIDE' ENTERED AT 09:50:31 ON 31 MAY 2006

FILE 'AGRICOLA, MEDLINE, CAPIUS, BIOSIS' ENTERED AT 09:52:39 ON 31 MAY 2006

L11 10 S L5 AND (STERO? OR KDA OR DA OR ZN)  
L12 17 S L5 AND (STER? OR OPTI? OR KDA OR DA OR ZN)

FILE 'STNGUIDE' ENTERED AT 09:55:13 ON 31 MAY 2006

	Type	L #	Hits	Search Text
1	BRS	L1	2856	rhodococcus
2	BRS	L2	235	l1 and (alcohol near2 dehydrogenase)
3	BRS	L3	29	l2 and ruber
4	BRS	L4	26	l2 and (rhodococcus near2 ruber)
5	BRS	L5	2	(alcohol near2 dehydrogenase) near10 (rhodococcus near2 ruber)
6	BRS	L6	16	(alcohol near2 dehydrogenase) near10 (rhodococcus )

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Search Protein for txid1830[Organism:noexp] AND dehydrogenase Preview Go C

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- Search numbers may not be continuous; all searches are represented.
- Click on query # to add to strategy

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	#17 Search txid1830[Organism:noexp] AND dehydrogenase	12:33:03	<a href="#">14</a>
	#16 Search txid1830[Organism:noexp]	12:32:59	<a href="#">58</a>
	#13 Protein Links for PubMed (Select 10531651)	12:31:11	<a href="#">2</a>

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May 22 2006 06:31:57

RESULT 1  
 US-10-004-115B-34  
 ; Sequence 34, Application US/10004115B  
 ; Patent No. 6884607  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ASAKO, HIROYUKI  
 ; APPLICANT: MATSUMURA, KENJI  
 ; APPLICANT: SHIMIZU, MASATOSHI  
 ; APPLICANT: ITO, NOBUYA  
 ; APPLICANT: WAKITA, RYUHEI  
 ; TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE  
 ; TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE  
 ; FILE REFERENCE: 7372-72249  
 ; CURRENT APPLICATION NUMBER: US/10/004,115B  
 ; CURRENT FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: JP 2000-372704  
 ; PRIOR FILING DATE: 2000-12-07  
 ; PRIOR APPLICATION NUMBER: JP 2001-006144  
 ; PRIOR FILING DATE: 2001-01-15  
 ; PRIOR APPLICATION NUMBER: JP 2001-026594  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: JP 2001-175175  
 ; PRIOR FILING DATE: 2001-06-11  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO 34  
 ; LENGTH: 348  
 ; TYPE: PRT  
 ; ORGANISM: Corynebacterium sp.

US-10-004-115B-34

Query Match 64.9%; Score 1152.5; DB 2; Length 348;  
 Best Local Similarity 63.6%; Pred. No. 1.8e-101;  
 Matches 220; Conservative 40; Mismatches 85; Indels 1; Gaps 1;

Qy	1 MKAVQYTEIGSEPVVVDIPTPTPGPGEILLKVTAAAGLCHSDIFVMDMPAAQYAYGLPLTL 60
Db	1 MKAIQYTRIGAEPELTEIPKPEPGPGEVLLEVTAAGVCHSDDFIMSLPEEQYTYGLPLTL 60
Qy	61 GHEGVGTVAELGEGVTGFGVGDAVAVYGPWCGCACHACARGRENYCTRAADLGITPPGLG 120
Db	61 GHEGAGKVAAVGEGVEGLDIGTNVVVYGPWCGNCWHCSQGLENYCSRAQELGINPPGLG 120
Qy	121 SPGSMAEYMIVDSARHLVPIGDLDPVAAAPLTDAGLTPYHAISRVLPLPGPGSTAVVIGV 180
Db	121 APGALAEFMIVDSPRHLVPIGDLDPVKTVPLTDAGLTPYHAIKRSLPKLRGGSYAVVIGT 180
Qy	181 GGLGHVGIQILRAVSAARVIAVDLDDDRLLALAREVGADAALKSGAGAADAIRELTGGQGA 240
Db	181 GGLGHVAIQLLRHLAAATVIALDVSADKLELATKVGAEVVLSDKAAENVRKITGSQGA 240
Qy	241 TAVFDFVGAQSTIDTAQQVAVDGHISVVGIIHAG-AHAKVGFMI PFGASVVT PYWGTRS 299
Db	241 ALVLDFVGYQPTIDTAMAVAGVGS DVTIVGIGDGQAHAKVGFQSPYEASVTVPYWGARN 300
Qy	300 ELMEVVALARAGRLDIHTETFTLDEGPAA YRRLREGSIRGRGVVVP 345
Db	301 ELIELIDLAHAGIFDISVETFSLDNGAEAYRRLAAGTLSGRAVVVP 346

RESULT 4

Q65YQ4\_9NOCA

ID Q65YQ4\_9NOCA PRELIMINARY; PRT; 348 AA.

AC Q65YQ4;

DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.

DT 25-OCT-2004, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE Phenylacetaldehyde reductase.

GN Name=par;

OS Rhodococcus sp. ST-10.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.

OX NCBI\_TaxID=85582;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ST-10;

RX PubMed=16085867; DOI=10.1128/AEM.71.8.4713-4720.2005;

RA Makino Y., Inoue K., Dairi T., Itoh N.;

RT "Engineering of Phenylacetaldehyde Reductase for Efficient Substrate Conversion in Concentrated 2-Propanol.";

RL Appl. Environ. Microbiol. 71:4713-4720(2005).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ST-10;

RX MEDLINE=20000646; PubMed=10531651; DOI=10.1007/s002530051536;

RA Wang J., Sakakibara M., Liu J., Dairi T., Itoh N.;

RT "Cloning, sequence analysis, and expression in Escherichia coli of the gene encoding phenylacetaldehyde reductases from styrene-assimilating Corynebacterium sp. ST-10.";

RL Appl. Microbiol. Biotechnol. 52:386-392(1999).

CC -!- COFACTOR: Zinc (By similarity).

CC -----

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CC -----

DR EMBL; AB190261; BAD51480.1; -; Genomic\_DNA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR InterPro; IPR013154; ADH\_N.

DR InterPro; IPR002085; ADH\_Sf\_Zn.

DR InterPro; IPR002328; ADH\_Zn.

DR InterPro; IPR013149; ADH\_Zn\_bd.

DR PANTHER; PTHR11695; Adh\_zn\_family; 1.

DR PROSITE; PS00059; ADH\_ZINC; 1.

KW Metal-binding; NAD; Oxidoreductase; Zinc.

SQ SEQUENCE 348 AA; 36222 MW; 57568097CF806BEB CRC64;

Query Match 64.9%; Score 1152.5; DB 2; Length 348;  
 Best Local Similarity 63.6%; Pred. No. 6.9e-66;  
 Matches 220; Conservative 40; Mismatches 85; Indels 1; Gaps 1;

Qy 1 MKAVQYTEIGSEPVVVDIPTPTPGPGEILLKVTAAGLCHSDIFVMDMPAAQYAYGLPLTL 60  
 ||||:|||| |||:|| :||| ||||||:||:||||||:|||| ||:|| :|| |||||||||  
 Db 1 MKAIQYTRIGAEPELTEIPKPEPGPGEVLLEVTAAGVCHSDDFIMSLPEEQTYGLPLTL 60

Qy 61 GHEGVGTVAELGEGVTGFGVGDAVAVYGPWCGCACHACARGRENYCTRAADLGITPPGLG 120  
 ||||| ||| :||||| | :|| | ||||||||| | ||::| ||||:|| :||| |||||  
 Db 61 GHEGAGKVAAVGEGVEGLDIGTNVVVYGPWCGNCWHCSQGLENYCSRAQELGINPPGLG 120

Qy 121 SPGSMAEYMIIVDSARHLVPIGDLDPVAAAPLTDAGLTPYHAISRVLPLPGPGSTAVVIGV 180

Db :||:||:|||| ||||||||| ||||||||| | || | || |||||  
121 APGALAEFMIVDSPRHLVPIGDLDPVKTVPLTDAGLTPYHAIKRSLPKLRGGSYAVVIGT 180

Qy 181 GGLGHVGIQILRAVSAARVIAVDLDDDRLLALAREVGADAAVKSGAGAADAIRELTGGQGA 240  
||| ||| ||:|| :||| ||:||: |:| || :||| | | ||: :||:|| | |||

Db 181 GGLGHVAIQLLRHLAAATVIALDVSADKLELATKVGAEVVILSDKAAENVRKITGSQGA 240

Qy 241 TAVFDFVGAQSTIDTAQQVVAVDGHISVVGIGHAG-AHAKVGFFMIPFGASVVTPYWGTRS 299  
| |||| | ||||| | | :::||| | |||||||| |: ||| |||| |:  
Db 241 ALVLDFVGYQPTIDTAMAVAGVGSVTVIGIGDGQAHAKVGFFQSPYEASVTVPYWGARN 300

Qy 300 ELMEVVVALARAGRLDIHTETFTLDEGPAAAYRRLREGSIRGRGVVVP 345  
||:||:| ||| || ||:|| | ||||| |::| || |||||

Db 301 ELIELIDLAHAGIFDISVETFSLDNGAEAYRRLAAGTLSGRAVVVP 346

RESULT 1  
US-09-252-991A-26632  
; Sequence 26632, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26632  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26632

Query Match 90.7%; Score 39; DB 2; Length 233;  
Best Local Similarity 80.0%; Pred. No. 17;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGAGAADAXR 10  
:||||||| |  
Db 18 AGAGAADARR 27

Database : PIR\_80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35	81.4	123	2	H81235	50S ribosomal prot
2	34	79.1	255	2	JC7264	CCAAT-enhancer bin
3	34	79.1	263	2	B75361	WD-repeat family p
4	34	79.1	525	2	AF3274	hypothetical prote
5	34	79.1	547	1	S51475	cytochrome P450 cy
6	34	79.1	602	2	H87503	phosphogluconate d
7	34	79.1	741	2	D75500	ATP-dependent Clp
8	34	79.1	1335	2	H75511	DNA polymerase III
9	33	76.7	299	2	F75295	hypothetical prote
10	33	76.7	370	2	A60089	transforming prote
11	33	76.7	397	2	T35609	whiE protein I - S
12	33	76.7	428	2	S17817	bacteriochlorophyl
13	33	76.7	461	2	T51030	probable acetylorn
14	33	76.7	463	2	T34841	probable bifunctio
15	33	76.7	588	2	AC0611	transport ATP-bind
16	33	76.7	588	2	B85614	hypothetical prote
17	33	76.7	588	2	D90750	hypothetical prote
18	33	76.7	588	2	F64827	ABC-type

Database : UniProt\_7.2:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	42	97.7	346	2	Q8KLT9_9NOCA	Q8klt9 rhodococcus
2	39	90.7	478	2	Q82F52_STRAW	Q82f52 streptomyce
3	38	88.4	557	2	Q2T4A0_BURTH	Q2t4a0 burkholderi
4	38	88.4	581	2	Q5KGT5_CRYNE	Q5kgt5 cryptococcu
5	38	88.4	613	2	Q55SE1_CRYNE	Q55sel cryptococcu
6	38	88.4	964	2	Q4KXA8_LEIME	Q4kxa8 leishmania
7	37	86.0	737	2	Q8LTQ2_9CAUD	Q8ltq2 lactococcus
8	36	83.7	241	2	Q651U8_ORYSA	Q651u8 oryza sativ
9	36	83.7	248	2	Q84R34_ORYSA	Q84r34 oryza sativ
10	36	83.7	379	2	Q3GCC8_9FIRM	Q3gcc8 syntrophomo
11	35	81.4	73	2	Q7R475_GIALA	Q7r475 giardia lam
12	35	81.4	81	2	Q341E1_RHOPA	Q341e1 rhopospseudo
13	35	81.4	122	1	RL7_NEIMA	POa0x0 neisseria m
14	35	81.4	122	1	RL7_NEIMB	POa0x1 neisseria m
15	35	81.4	123	2	Q5F5R4_NEIG1	Q5f5r4 neisseria g
16	35	81.4	132	2	Q4DER8_TRYCR	Q4der8 trypanosoma
17	35	81.4	135	2	Q4D9Q6_TRYCR	Q4d9q6 trypanosoma
18	35	81.4	296	2	P72540_STRPR	

RESULT 1  
 Q8KLT9\_9NOCA  
 ID Q8KLT9\_9NOCA PRELIMINARY; PRT; 346 AA.  
 AC Q8KLT9;  
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 19.  
 DE Secondary alcohol dehydrogenase (EC 1.1.1.1).  
 GN Name=sadh;  
 OS Rhodococcus ruber.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Nocardiaceae; Rhodococcus.  
 OX NCBI\_TaxID=1830;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=219;  
 RA Tamak C., Plattner H., Hummel W., Diekmann H., Meens J.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
 CC -!- COFACTOR: Zinc (By similarity).  
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 CC -----  
 DR EMBL; AJ491307; CAD36475.1; -; Genomic\_DNA.  
 DR HSSP; Q59096; 1F8F.  
 DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.  
 DR GO; GO:0046872; F:metal ion binding; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR InterPro; IPR013154; ADH\_N.  
 DR InterPro; IPR002085; ADH\_Sf\_Zn.  
 DR InterPro; IPR002328; ADH\_Zn.  
 DR InterPro; IPR013149; ADH\_Zn\_bd.  
 DR InterPro; IPR002110; ANK.  
 DR PANTHER; PTHR11695; Adh\_zn\_family; 1.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR PROSITE; PS00059; ADH\_ZINC; 1.  
 KW Metal-binding; NAD; Oxidoreductase; Zinc.  
 SQ SEQUENCE 346 AA; 35449 MW; F885D8B0F7E6C1CC CRC64;

Query Match 97.7%; Score 42; DB 2; Length 346;  
 Best Local Similarity 90.0%; Pred. No. 27;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGAGAADAXR 10  
 |||||||| |  
 Db 223 SGAGAADAIR 232

Database : A\_Geneseq\_8:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1775	100.0	345	9	ADY85204	Ady85204 Rhodococc
2	1188.5	67.0	346	9	ADZ03703	Adz03703 Streptomy
3	1152.5	64.9	348	8	ADL18256	Adl18256 Corynebac
4	1152.5	64.9	348	9	ADV69575	Adv69575 Corynebac
5	1151.5	64.9	348	7	ADF53768	Adf53768 Alcohol d
6	1150.5	64.8	348	9	AED84856	Aed84856 Alcohol d
7	1145.5	64.5	348	9	AED84855	Aed84855 Alcohol d
8	1100.5	62.0	344	8	ADN25583	Adn25583 Bacterial
9	1061.5	59.8	384	8	ADK70245	Adk70245 Corynebac
10	1061.5	59.8	385	5	AAO21525	Aao21525 385-mer C
11	1061.5	59.8	385	5	ABB77974	Abb77974 Amino aci
12	1061.5	59.8	385	7	ADE39627	Ade39627 Corynebac
13	1061.5	59.8	385	8	ADF88657	Adf88657 3-quinucl
14	1061.5	59.8	385	8	ADK82546	Adk82546 Isomerase
15	1061.5	59.8	385	8	ADM46684	Adm46684 385 amino
16	1061.5	59.8	385	8	ADM46565	Adm46565 Corynebac
17	916.5	51.6	327	8	ADN25512	Adn25512 Bacterial
18	577	32.5	162	9	AED84825	Aed84825 Alcohol d
19	559	31.5	161	9	AED84826	Aed84826 Alcohol d
20	556	31.3	162	9	AED84823	Aed84823 Alcohol d
21	533	30.0	341	9	ADZ47402	Adz47402 341 amino
22	480.5	27.1	359	8	ADS44521	Ads44521 Bacterial
23	476	26.8	128	9	AED84824	

Database : Issued\_Patents\_AA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1152.5	64.9	348	2	US-10-004-115B-34	Sequence 34, Appl
2	1061.5	59.8	385	2	US-09-984-334-1	Sequence 1, Appl
3	481.5	27.1	352	2	US-09-504-358-18	Sequence 18, Appl
4	481.5	27.1	352	2	US-09-954-314-18	Sequence 18, Appl
5	481.5	27.1	352	2	US-10-230-562-18	Sequence 18, Appl
6	465.5	26.2	352	2	US-09-648-004-24	Sequence 24, Appl
7	465.5	26.2	352	2	US-10-272-419-24	Sequence 24, Appl
8	463.5	26.1	381	2	US-09-248-796A-20906	Sequence 20906, A
9	422.5	23.8	336	1	US-08-713-254-2	Sequence 2, Appl
10	422.5	23.8	336	2	US-08-855-767-2	Sequence 2, Appl
11	414.5	23.4	346	2	US-09-489-039A-9885	Sequence 9885, Ap
12	403	22.7	344	2	US-09-134-001C-5343	Sequence 5343, Ap
13	394.5	22.2	465	2	US-09-252-991A-18919	Sequence 18919, A
14	374.5	21.1	375	2	US-09-134-000C-5937	Sequence

Database : Published\_Applications\_AA\_Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1775	100.0	345	4	US-10-666-205-48	Sequence 48, Appl
2	1713	96.5	346	6	US-11-087-099-9022	Sequence 9022, Ap
3	1152.5	64.9	348	5	US-10-617-034A-1	Sequence 1, Appli
4	1151.5	64.9	348	6	US-11-188-298-13982	Sequence 13982, A
5	1100.5	62.0	344	4	US-10-369-493-8236	Sequence 8236, Ap
6	1061.5	59.8	385	3	US-09-984-334-1	Sequence 1, Appli
7	1061.5	59.8	385	4	US-10-004-115A-34	Sequence 34, Appl
8	1061.5	59.8	385	4	US-10-327-108-1	Sequence 1, Appli
9	1061.5	59.8	385	5	US-10-920-239-34	Sequence 34, Appl
10	1061.5	59.8	385	6	US-11-087-099-1453	Sequence 1453, Ap
11	1061.5	59.8	385	6	US-11-188-298-1461	Sequence 1461, Ap
12	933.5	52.6	360	6	US-11-188-298-5305	Sequence 5305, Ap
13	916.5	51.6	327	4	US-10-369-493-8165	Sequence 8165, Ap
14	606	34.1	341	4	US-10-156-761-8932	Sequence

Database : PIR\_80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	526	29.6	344	2	D90325	alcohol dehydrogen
2	480.5	27.1	359	2	C72533	probable alcohol d
3	472	26.6	347	1	S51120	alcohol dehydrogen
4	465	26.2	347	1	A44245	alcohol dehydrogen
5	455.5	25.7	349	2	B90285	alcohol dehydrogen
6	451.5	25.4	340	2	T37030	alcohol dehydrogen
7	445.5	25.1	236	2	T36399	probable alcohol d
8	442	24.9	346	2	H81915	probable alcohol d
9	442	24.9	348	2	H81186	probable alcohol d
10	419.5	23.6	336	2	AH0672	alcohol dehydrogen
11	419	23.6	365	2	T36806	probable alcohol d
12	417.5	23.5	342	2	H97434	alcohol dehydrogen
13	417.5	23.5	342	2	AD2653	alcohol dehydrogen
14	415	23.4	346	1	A64901	alcohol dehydrogen
15	415	23.4	346	2	G85728	alcohol dehydrogen

Database : UniProt\_7.2:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1713	96.5	346	2	Q8KLT9_9NOCA	Q8klt9 rhodococcus
2	1188.5	67.0	346	2	Q9S5E6_STRCO	Q9s5e6 streptomyce
3	1168.5	65.8	348	2	Q415U1_KINRA	Q415u1 kineococcus
4	1152.5	64.9	348	2	Q65YQ4_9NOCA	Q65yq4 rhodococcus
5	1151.5	64.9	348	2	Q6YBW1_RHOER	Q6ybw1 rhodococcus
6	1151.5	64.9	348	2	Q9ZN85_9NOCA	Q9zn85 rhodococcus
7	1150.5	64.8	346	2	Q5YTY4_NOCFA	Q5yty4 nocardia fa
8	1100.5	62.0	348	2	Q47L68_THEFY	Q47l68 thermobifid
9	933.5	52.6	360	2	Q47PU4_THEFY	Q47pu4 thermobifid
10	881	49.6	343	2	Q46N63_RALEJ	Q46n63 ralstonia e
11	856.5	48.3	354	2	Q3H4C5_9ACTO	Q3h4c5 nocardioide
12	742.5	41.8	347	2	Q5YR32_NOCFA	Q5yr32 nocardia fa
13	704	39.7	359	2	Q5YXH9_NOCFA	Q5yxh9 nocardia fa
14	606	34.1	341	2	Q82NBO_STRAW	Q82nb0 streptomyce
15	579	32.6	347	2	Q3X235_9ACTN	Q3x235 rubrobacter
16	566	31.9	341	2	Q4J706_SULAC	Q4j706 sulfolobus
17	555.5	31.3	353	2	Q3WYQ7_9ACTN	Q3wyq7 rubrobacter
18	553	31.2	341	2	Q8CK64_STRCO	Q8ck64 streptomyce
19	552	31.1	341	2	Q2JA11_9ACTO	Q2ja11 frankia

RESULT 1

Q8KLT9\_9NOCA

ID Q8KLT9\_9NOCA PRELIMINARY; PRT; 346 AA.

AC Q8KLT9;

DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.

DT 07-FEB-2006, entry version 19.

DE Secondary alcohol dehydrogenase (EC 1.1.1.1).

GN Name=sadh;

OS Rhodococcus ruber.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.

OX NCBI\_TaxID=1830;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=219;

RA Tamak C., Plattner H., Hummel W., Diekmann H., Meens J.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

CC -!- COFACTOR: Zinc (By similarity).

CC -----

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CC -----

DR EMBL; AJ491307; CAD36475.1; -; Genomic\_DNA.

DR HSSP; Q59096; 1F8F.

DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR InterPro; IPR013154; ADH\_N.

DR InterPro; IPR002085; ADH\_Sf\_Zn.

DR InterPro; IPR002328; ADH\_Zn.

DR InterPro; IPR013149; ADH\_Zn\_bd.

DR InterPro; IPR002110; ANK.

DR PANTHER; PTHR11695; Adh\_zn\_family; 1.

DR PRINTS; PR01415; ANKYRIN.

DR PROSITE; PS00059; ADH\_ZINC; 1.

KW Metal-binding; NAD; Oxidoreductase; Zinc.

SQ SEQUENCE 346 AA; 35449 MW; F885D8B0F7E6C1CC CRC64;

Query Match 96.5%; Score 1713; DB 2; Length 346;  
 Best Local Similarity 95.7%; Pred. No. 8.1e-102;  
 Matches 330; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MKAVQYTEIGSEPVVVDIPTPTPGPGEILLKVTAAAGLCHSDIFVMDMPAAQYAYGLPLTL 60  
 ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 1 MKALQYTEIGSEPVVVDVPTPAPGPGEILLKVTAAAGLCHSDIFVMDMPAEQYIYGLPLTL 60

Qy 61 GHEGVGTVVAELGEGVTGFGVGDAVAVYGPWCGGACHACARGRENYCTRAADLGITPPGLG 120  
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 61 GHEGVGTVVAELGAGVTGFETGDAVAVYGPWCGGACHACARGRENYCTRAELGITPPGLG 120

Qy 121 SPGSMAEYMICVDSARHLVPIGDLDPVAAAPLTDAGLTPYHAISRVPLLLPGPGSTAVVIGV 180  
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 121 SPGSMAEYMICVDSARHLVPIGDLDPVAAVPLTDAGLTPYHAISRVPLLLPGPGSTAVVIGV 180

Qy 181 GGLGHVGIQILRAVSAARVIAVLDLDDRLLALAREVGADAAVKSGAGAADAIRELTGGQGA 240  
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 181 GGLGHVGIQILRAVSAARVIAVLDLDDRLLALAREVGADAAVKSGAGAADAIRELTGGEGA 240

Qy 241 TAVFDFVGAQSTIDTAQQVVAVDGHISVVGIGHAGAHAKVGFIMIPFGASVVT PYWGTRSE 300

Db :|||||||||||||||||:|||||||||||||||||||||||||  
241 TAVDFVGAQSTIDTAQQVVAIDGHISVVGIHAGAHAKVGFMI PFGASVVT PYWGTRSE 300

Qy ||:|| ||||||||||||||||| |||||||||||||||||  
301 LMEVVALARAGRLDIHTETFTLDEGPAAAYRRLREGSIRGRGVVVP 345

Db ||:|| ||||||||||||||||| |||||||||||||||||  
301 LMDVVDLARAGRLDIHTETFTLDEGPTAYRRLREGSIRGRGVVVP 345

RESULT 4

Q65YQ4\_9NOCA

ID Q65YQ4\_9NOCA PRELIMINARY; PRT; 348 AA.

AC Q65YQ4;

DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.

DT 25-OCT-2004, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE Phenylacetaldehyde reductase.

GN Name=par;

OS Rhodococcus sp. ST-10.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.

OX NCBI\_TaxID=85582;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ST-10;

RX PubMed=16085867; DOI=10.1128/AEM.71.8.4713-4720.2005;

RA Makino Y., Inoue K., Dairi T., Itoh N.;

RT "Engineering of Phenylacetaldehyde Reductase for Efficient Substrate Conversion in Concentrated 2-Propanol.";

RL Appl. Environ. Microbiol. 71:4713-4720(2005).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ST-10;

RX MEDLINE=20000646; PubMed=10531651; DOI=10.1007/s002530051536;

RA Wang J., Sakakibara M., Liu J., Dairi T., Itoh N.;

RT "Cloning, sequence analysis, and expression in Escherichia coli of the gene encoding phenylacetaldehyde reductases from styrene-assimilating Corynebacterium sp. ST-10.";

RL Appl. Microbiol. Biotechnol. 52:386-392(1999).

CC -!- COFACTOR: Zinc (By similarity).

CC -----

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CC -----

DR EMBL; AB190261; BAD51480.1; -; Genomic\_DNA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR InterPro; IPR013154; ADH\_N.

DR InterPro; IPR002085; ADH\_Sf\_Zn.

DR InterPro; IPR002328; ADH\_Zn.

DR InterPro; IPR013149; ADH\_Zn\_bd.

DR PANTHER; PTHR11695; Adh\_zn\_family; 1.

DR PROSITE; PS00059; ADH\_ZINC; 1.

KW Metal-binding; NAD; Oxidoreductase; Zinc.

SQ SEQUENCE 348 AA; 36222 MW; 57568097CF806BEB CRC64;

Query Match 64.9%; Score 1152.5; DB 2; Length 348;  
 Best Local Similarity 63.6%; Pred. No. 6.9e-66;  
 Matches 220; Conservative 40; Mismatches 85; Indels 1; Gaps 1;

Qy 1 MKAVQYTEIGSEPVVVDIPTPTPGPGEILLKVTAAAGLCHSDIFVMDMPAAQYAYGLPLTL 60  
 |||:||| ||:|| :|| | |||||:||:|||||:||||| :|| :| || |||||||  
 Db 1 MKAIQYTRIGAEPELTEIPKPEPGPGEVLLEVTAAGVCHSDDFIMSLPEEQTYGLPLTL 60

Qy 61 GHEGVGTVAELGEGVTGFGVGDAVAVYGPWCGCACHACARGRENYCTRAADLGITPPGLG 120  
 |||| | || :|||| | :|| | |||||||| | ||:| ||||:|| :||| |||||  
 Db 61 GHEGAGKVAAVGEGVEGLDIGTNVVVYGPWCGCNCWHCSQGLENYCSRAELGINPPGLG 120

Qy 121 SPGSMAEYMIIVDSARHLVPIGDLDPVAAAPLTDAGLTPYHAISRVLPLGPGSTAVVIGV 180

Db :||:||:|||| ||||||||||| ||||||||||| | || | || |||||  
121 APGALAEFMIVDSPRHLVPIGDLDPVKTVPLTDAGLTPYHAIKRSLPKLRGGSYAVVIGT 180

Qy 181 GGLGHVGIQILRAVSAARVIAVDLDDDRLLALAREVGADAALKSGAGAADAIRELTGGQGA 240  
||| ||| ||:|| :||| ||:||: ||| :||| ||| ||| ||: ||:|| |||

Db 181 GGLGHVAIQLLRHLSAATVIALDVSADKLELATKVGAEVVLSDKDAAENVRKITGSQGA 240

Qy 241 TAVFDFVGAQSTIDTAQQVVAVDGHISVVGIGHAG-AHAKVGFIMIPFGASVVT PYWGTRS 299  
| |||| | ||||| | | :::||| | |||||||| |: ||| |||| |:

Db 241 ALVLDFVGYQPTIDTAMAVAGVGSVTIVGIGDGQAHAKVGFQSPYEASVTVPYWGARN 300

Qy 300 ELMEVVALARAGRLDIHTETFTLDEGPAAAYRRLREGSIRGRGVVVP 345  
||:||:||| ||| ||| ||:|| | ||||| |::||| |||

Db 301 ELIELIDLAHAGIFDISVETFSLDNGAEAYRRLAAGTLSGRAVVVP 346

Database : A\_Geneseq\_8:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query			Description	
		Match	Length	DB	ID	
1	9	100.0	10	7	ADD44401	Add44401 Rhodococc
2	9	100.0	10	9	ADY85159	Ady85159 Rhodococc
3	8	88.9	248	8	ADX93553	Adx93553 Plant ful
4	8	88.9	267	8	ADX87812	Adx87812 Plant ful
5	8	88.9	268	8	ADX88645	Adx88645 Plant ful
6	8	88.9	345	9	ADY85204	Ady85204 Rhodococc
7	8	88.9	799	7	ABM88577	Abm88577 Rice abio
8	7	77.8	106	3	AAG26730	Aag26730 Zea mays
9	7	77.8	123	3	AAy81132	Aay81132 Neisseria
10	7	77.8	123	3	AAy81131	Aay81131 Neisseria
11	7	77.8	123	6	ABP80703	Abp80703 N. gonorr
12	7	77.8	123	6	ABU37479	Abu37479 Protein e
13	7	77.8	123	6	ABU37710	Abu37710 Protein e
14	7	77.8	123	8	ADP08183	Adp08183 Neisseria
15	7	77.8	137	3	AAG26729	Aag26729 Zea mays
16	7	77.8	137	8	ADQ09964	Adq09964 Borrelia
17	7	77.8	171	7	ABO71893	Abo71893 Pseudomon

Database : Issued\_Patents\_AA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	7	77.8	171	2	US-09-252-991A-20639	Sequence 20639, A
2	7	77.8	233	2	US-09-252-991A-26632	Sequence 26632, A
3	7	77.8	298	2	US-09-252-991A-22985	Sequence 22985, A
4	7	77.8	414	2	US-09-252-991A-17165	Sequence 17165, A
5	7	77.8	485	2	US-09-252-991A-24868	Sequence 24868, A
6	7	77.8	614	2	US-09-252-991A-20210	Sequence 20210, A
7	7	77.8	717	2	US-09-252-991A-22029	Sequence 22029, A
8	7	77.8	743	2	US-09-252-991A-28327	Sequence 28327, A
9	6	66.7	118	2	US-08-301-162-10	Sequence 10, Appl
10	6	66.7	118	2	US-09-461-240-10	Sequence 10, Appl
11	6	66.7	118	2	US-09-968-927-10	Sequence 10, Appl
12	6	66.7	133	2	US-09-252-991A-30896	Sequence 30896, A
13	6	66.7	139	2	US-09-270-767-35479	Sequence 35479, A
14	6	66.7	139	2	US-09-270-767-50696	Sequence 50696, A
15	6	66.7	150	2	US-09-252-991A-29818	Sequence 29818, A
16	6	66.7	169	2	US-09-252-991A-26193	Sequence 26193, A

Database : PIR\_80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result	Query				Description	
No.	Score	Match	Length	DB	ID	Description
1	7	77.8	123	2	H81235	50S ribosomal prot
2	7	77.8	255	2	JC7264	CCAAT-enhancer bin
3	7	77.8	263	2	B75361	WD-repeat family p
4	6	66.7	109	1	R6BY11	acidic ribosomal p
5	6	66.7	112	2	B43601	LSR2 T-cell antige
6	6	66.7	137	2	AD3645	flagella basal bod
7	6	66.7	161	2	E70867	hypothetical prote
8	6	66.7	183	2	T51910	hypothetical prote
9	6	66.7	184	2	C95930	conserved hypothet

Database : UniProt\_7.2:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	%	Description
						Query	
1	8	88.9	346	2	Q8KLT9_9NOCA		Q8klt9 rhodococcus
2	8	88.9	557	2	Q2T4A0_BURTH		Q2t4a0 burkholderi
3	8	88.9	581	2	Q5KGT5_CRYNE		Q5kgt5 cryptococcus
4	8	88.9	613	2	Q55SE1_CRYNE		Q55sel cryptococcus
5	7	77.8	73	2	Q7R475_GIALA		Q7r475 giardia lam
6	7	77.8	98	2	Q7Y1Q2_MAIZE		Q7y1q2 zea mays (m)
7	7	77.8	99	2	Q4P9Q4_USTMA		Q4p9q4 ustilago ma
8	7	77.8	122	1	RL7_NEIMA		P0a0x0 neisseria m
9	7	77.8	122	1	RL7_NEIMB		P0a0x1